



SEQUENCE LISTING

<110> REVEL, Michel
CHEBATH, Judith
LAPIDOT, Tsvee
KOLLET, Orit

<120> CHIMERIC INTERLEUKIN-6 SOLUBLE RECEPTOR/LIGAND PROTEIN, ANALOGS
THEREOF AND USES THEREOF

<130> REVEL=15

<140> 09/462,416

<141> 2000-04-13

<150> PCT/IL98/00321

<151> 1998-07-09

<150> IL 121284

<151> 1997-07-10

<150> IL 122818

<151> 1997-12-30

<160> 12

<170> PatentIn version 3.1

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<212> PRT

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Glu Phe Gly Ala Gly Leu Val Leu Gly Gly Gln Phe Met
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ctagtgggcc cggggtggcg gg

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gactagtagc tatgaactcc ttctc

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agggccattt gccgaagagc c

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gatccgggcg gcgggggagg ggggcccggg c

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Gly Gly Gly Gly Asp Pro Gly Gly Gly Gly Gly Gly Pro Gly
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Met Leu Ala Val Gly Cys Ala Leu Leu Ala¹ Ala Leu Leu Ala Ala Pro
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Gly Ala Ala Leu¹ Ala Pro Arg Arg Cys Pro Ala Gln Glu² Val¹ Ala Arg
20 25 30

Gly Val Leu¹ Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
35 40 45

Gly Val¹ Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
50 55 60

Pro¹ Ala Ala Gly Ser His¹ Pro Ser Arg Trp Ala¹ Gly Met Gly Arg Arg
65 70 75 80

Leu Leu Leu Arg Ser Val Gln Leu His Asp¹ Ser Gly Asn Tyr Ser Cys
85 90 95

Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
100 105 110

Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
115 120 125

Asn Val¹ Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
130 135 140

Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
145 150 155 160

Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu¹ Ser Gln Lys Phe Ser¹ Cys
165 170 175

Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val¹ Ser Met
180 185 190

Cys Val Ala¹ Ser Ser Val Gly Ser¹ Lys Phe Ser Lys Thr¹ Gln Thr Phe
195 200 205

Gln Gly¹ Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala¹ Asn Ile Thr Val
210 215 220

Thr¹ Ala Val Ala Arg Asn¹ Pro Arg Trp Leu Ser¹ Val Thr Trp Gln Asp¹
225 230 235 240

Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
245 250 255

Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
260 265 270

Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
275 280 285

Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
290 295 300

Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
305 310 315 320

Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr
325 330 335

Asn Lys Asp Asp Asp Asn Ile Leu Phe Arg Asp Ser Ala Asn Ala Thr
340 345 350

Ser Leu Pro Val Glu Phe Met Pro Val Pro Pro Gly Glu Asp Ser Lys
355 360 365

Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile
370 375 380

Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys
385 390 395 400

Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu
405 410 415

Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys
420 425 430

Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr
435 440 445

Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe
450 455 460

Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val
465 470 475 480

Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr
485 490 495

Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala
500 505 510

Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser
515 520 525

Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
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Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Pro
20 25 30

Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr
35 40 45

Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile
50 55 60

Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser
65 70 75 80

Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala
85 90 95

Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu
100 105 110

Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr
115 120 125

51

Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln
130 135 140

Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn
145 150 155 160

Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu
165 170 175

Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His
180 185 190

Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala
195 200 205

Leu Arg Gln Met Gly Gly Gly Gly Asp Pro Gly Gly Gly Gly Gly Gly
210 215 220

Pro Gly Val Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser
225 230 235 240

Pro Leu Ser Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser
245 250 255

Leu Thr Thr Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro
260 265 270

Ala Glu Asp Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys
275 280 285

Phe Ser Cys Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile
290 295 300

Val Ser Met Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr
305 310 315 320

Gln Thr Phe Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn
325 330 335

Ile Thr Val Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr
340 345 350

Trp Gln Asp Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe
355 360 365

Glu Leu Arg Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met
370 375 380

Val Lys Asp Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly
385 390 395 400

Leu Arg His Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly
405 410 415

Glu Trp Ser Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu
420 425 430

Ser Arg Ser Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala
435 440 445

Leu Thr Thr Asn Lys Asp Asp Asp Asn Ile Leu Phe Arg Asp Ser Ala
450 455 460

Asn Ala Thr Ser Leu Pro Val
465 470

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<212> DNA
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<220>
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<400> 10
cagtacccga attcatgc

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<210> 11
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<212> DNA
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<400> 11
catggcccg ggcctectcc cccgccgcc g

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<212> DNA
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gatccccgcc accccgggcc ca

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